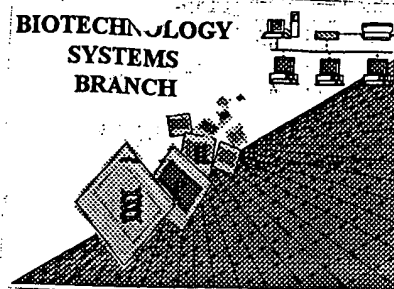


RAW SEQUENCE LISTING **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/725,906

Source: O/PE

Date Processed by STIC: 12/11/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

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SEQUENCE LISTING

Does Not Comply
Corrected Diskette Needed

(1) GENERAL INFORMATION:

(i) APPLICANT: LISA MCKERRACHER

(ii) TITLE OF INVENTION: Methods for making and delivering Rho-antagonist
tissue ← move up
central ← move up
adhesive formulations to the injured mammalian
and peripheral nervous systems and uses thereof

(iii) NUMBER OF SEQUENCES: 3

(iv) CORRESPONDENCE ADDRESS:

(A) ~~ADDRESSEE~~ BROULLETTE KOSIE
(B) STREET: 1100 RENE-LESVEQUE BLVD WEST
(D) ~~CT~~ ~~PROV~~ STATE: QUEBEC
(E) ~~CD~~ COUNTRY: CANADA
(F) ~~ET~~ ~~POSTAL~~ ZIP CODE: H3B 5C9

→ ADDRESSEE:

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: ASCII (TEXT)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ~~(vii)~~ ATTORNEY/AGENT INFORMATION:

(A) NAME: RONALD S. KOSIE
(B) ~~REGISTRATION NO.~~
(C) REFERENCE/DOCKET NO.: 06447-003-US-2

delete, since no response exists
→ spell out NUMBER

(A) TELEPHONE: ~~(D) TEL. NO.:~~ (514) 397 8500
(B) TELEFAX: ~~(E) FAX NO.:~~ (514) 397 8515

→ (ix) TELECOMMUNICATION INFORMATION:
(add heading)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: _____
(B) TYPE: _____
(C) STRANDEDNESS: _____
(D) TOPOLOGY: _____

These four headings REQUIRE
responses

(ii) MOLECULE TYPE:

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(vii) IMMEDIATE SOURCE:

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(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (D) OTHER INFORMATION:

(x) PUBLICATION INFORMATION:

- (A) AUTHORS:
- (B) TITLE:
- (C) JOURNAL:
- (D) VOLUME:
- (E) ISSUE:
- (F) PAGES:
- (G) DATE:
- (H) DOCUMENT NO.:
- (I) FILING DATE:
- (J) PUBLICATION DATE:
- (K) RELEVANT RESIDUES IN SEQ ID NO:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GTG GCG ACC CTT CCC AAA TCG GAT CTG GTT CCG CGT GGA TCC TCT AGA

invalid numbering

GTC GAC CTG CAG GCA TGC AAT GCT TAT TCC ATT AAT CAA AAG GCT TAT TCA

20

AAT ACT TAC CAG GAG TTT ACT AAT ATT GAT CAA GCA AAA GCT TGG GGT AAT

35

GCT CAG TAT AAA AAG TAT GGA CTA AGC AAA TCA GAA AAA GAA GCT ATA

55

GTA TCA TAT ACT AAA AGC GCT AGT GAA ATA AAT GGA AAG CTA AGA CAA

70

AAT AAG GGA GTT ATC AAT GGA TTT CCT TCA AAT TTA ATA AAA CAA GTT GAA

85

CTT TTA GAT AAA TCT TTT AAT AAA ATG AAG ACC CCT GAA AAT ATT ATG TTA

100

105

TTT AGA GGC GAC GAC CCT GCT TAT TTA GGA ACA GAA TTT CAA AAC ACT

120

CTT CTT AAT TCA AAT GGT ACA ATT AAT AAA ACG GCT TTT GAA AAG GCT AAA

135

140

GCT AAG TTT TTA AAT AAA GAT AGA CTT GAA TAT GGA TAT ATT AGT ACT TCA

150

155

TTA ATG AAT GTT TCT CAA TTT GCA GGA AGA CCA ATT ATT ACA AAA TTT AAA

170

175

GTA GCA AAA GGC TCA AAG GCA GGA TAT ATT GAC CCT ATT AGT GCT TTT CAG

185

190

*Per Sequence Rules,
insert the cumulative
base total at right
margin of each line.*

48

*per Sequence Rules, a MAXIMUM of 16 codons permitted
per line*

51

25

*fix
numbering*

75

only 16

codons

per line

125 allowed

09/725,906 3

GGA CAA CTT GAA ATG TTG CTT CCT AGA CAT AGT ACT TAT CAT ATA GAC GAT
205

210

ATG AGA TTG TCT TCT GAT GGT AAA CAA ATA ATA ATT ACA GCA ACA ATG
220 225

ATG GGC ACA GCT ATC AAT CCT AAA TAA
235

240

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:
(B) TYPE:
(C) STRANDEDNESS:
(D) TOPOLOGY:

insert response

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(ix) FEATURE:

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GGATCCTCTA GAGTCGACCT GCAGGCATGC AATGCTTATT CCAATTAATCA 50
AAAGGCTTAT TCAAATACTT ACCAGGAGTT TACTAATATT GATCAAGCAA 100
AAGCTTGGGG TAATGCTCAG TATAAAAAGT ATGGACTAAG CAAATCAGAA 150
AAAGAAGCTA TAGTATCATA TACTAAAAGC GCTAGTGAAA TAAATGGAAA 200
GCTAAGACAA AATAAGGGAG TTATCAATGG ATTCCTTCA AATTTAATAA 250
AACAAGTTGA ACTTTTAGAT AAATCTTTTA ATAAAATGAA GACCCCTGAA 300
AATATTATGT TATTTAGAGG CGACGACCT GCTTATTTAG GAACAGAATT 350
TCAAAACACT CTTCTTAATT CAAATGGTAC AATTAATAAA ACGGCTTTTG 400
AAAAGGCTAA AGCTAAGTTT TTAAATAAAG ATAGACTTGA ATATGGATAT 450
ATTAGTACTT CATTAATGAA TGTTTCTCAA TTTGCAGGAA GACCAATTAT 500
TACAAAATTT AAAGTAGCAA AAGGCTCAAA GGCAGGATAT ATTGACCCTA 550
TTAGTGCTTT TCAGGGACAA CTTGAAATGT TGCTTCCTAG ACATAGTACT 600
TATCATATAG ACGATATGAG ATTGTCTTCT GATGGTAAAC AAATAATAAT 650
TACAGCAACA ATGATGGGCA CAGCTATCAA TCCTAAATAA

690 ← insert

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: *insert response*
(B) TYPE: *insert response*
(C) STRANDEDNESS:
(D) TOPOLOGY: *insert response*

(vi) ORIGINAL SOURCE:

(A) ORGANISM:

(ix) FEATURE:

(D) OTHER INFORMATION:

since this appears to be an amino acid sequence, no need to insert (C) STRANDEDNESS: response; it is only required in nucleic acid sequence

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4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GSSRVDLQAC NAYSINQKAY SNTYQEFNTI DQAKAWGNAQ YKKYGLSKSE 50
 KEAIVSYTKS ASEINGKLRQ NKGVIINGFPS NLIKQVELLD KSFNKMKTPE
 NIMLFXGDDP AYLGTETQNT LLNSNGTINK TAFEKAKAKF LNXDRLEYGY
 ISTSLMNVSQ FAGRPITKF KVAKGSKAGY IDPISAFQGG LEMLLPRHST
 YHIDDMRLSS DGKQIIITAT MGMTAINPK

100

150

200

do not use one-letter amino acids in the
 Sequence Listing. Use three-letter
 amino acids, and number them under
every 5 amino acids. DO NOT use TAB
 codes between amino acids. Use space
 characters.

Please consult sample Sequence Listing
 (attached) for valid format.

(3) Computer: Apple Macintosh;
 (i) Operating System: Macintosh;
 (ii) Macintosh File Type: text with line termination
 (iii) Line Terminator: Pre-defined by text type file;
 (iv) Pagination: Pre-defined by text type file;
 (v) End-of-file: Pre-defined by text type file;
 (vi) Media: (A) Diskett—3.50 Inch, 400 Kb storage;
 (B) Diskette—3.50 inch, 800 Kb storage;
 (C) Diskette—3.50 inch, 1.4 Mb storage;
 (vii) Print Command: Use PRINT command from any Macintosh Application that processes text files, such as MacWrite or Teach Text;
 (4) Magnetic tape: 0.5 inch, up to 2400 feet;
 (i) Density: 1600 or 6250 bits per inch, 9 track;
 (ii) Format: raw, unblocked;
 (iii) Line Terminator: ASCII Carriage Return plus optional ASCII Line Feed;
 (iv) Pagination: ASCII Form Feed or Series of Line Terminators;
 (v) Print Command (Unix shell version given here as sample response—mt/dev/rmt0; lpr/dev/rmt0):
 (g) Computer readable forms that are submitted to the Office will not be returned to the applicant.
 (h) All computer readable forms shall have a label permanently affixed thereto on which has been hand printed or typed, a description of the format of the computer readable form as well as the name of the applicant, the title of the invention, the date on which the data were recorded on the computer readable form and the name and type of computer and operating system which generated the files on the computer readable form. If all of this information cannot be printed on a label affixed to the computer readable form, by reason of size or otherwise, the label shall include the name of the applicant and the title of the invention and a reference number, and the additional information may be provided on a container for the computer readable form with the name of the applicant, the title of the invention, the reference number and the additional information affixed to the container. If the computer readable form is submitted after the date of filing

under 35 U.S.C. 111, after the date of entry in the national stage under 35 U.S.C. 371 or after the time of filing; in the United States Receiving Office, an international application under the PCT, the labels mentioned herein must also include the date of the application and the application number, including series code and serial number.

§ 1.825 Amendments to or replacement of sequence listing and computer readable copy thereof.

(a) Any amendment to the paper copy of the "Sequence Listing" (§ 1.821(c)) must be made by the submission of substitute sheets. Amendments must be accompanied by a statement that indicates support for the amendment in the application, as filed, and a statement that the substitute sheets include no new matter. Such a statement must be a verified statement if made by a person not registered to practice before the Office.

(b) Any amendment to the paper copy of the "Sequence Listing," in accordance with paragraph (a) of this section, must be accompanied by a substitute copy of the computer readable form (§ 1.821(e)) including all previously submitted data with the amendment incorporated therein, accompanied by a statement that the copy in computer readable form is the same as the substitute copy of the "Sequence Listing." Such a statement must be a verified statement if made by a person not registered to practice before the Office.

(c) Any appropriate amendments to the "Sequence Listing" in a patent, e.g., by reason of reissue or certificate of correction, must comply with the requirements of paragraphs (a) and (b) of this section.

(d) If, upon receipt, the computer readable form is found to be damaged or unreadable, applicant must provide, within such time as set by the Commissioner, a substitute copy of the data in computer readable form accompanied by a statement that the substitute data is identical to that originally filed. Such a statement must be a verified statement if made by a person not registered to practice before the Office.

Appendix A—Sample Sequence Listing

(1) GENERAL INFORMATION:

(i) APPLICANT: Doe, Joan X. Doe, John Q
 (ii) TITLE OF INVENTION: Isolation and Characterization of a Gene Encoding a Protease from *Paramecium* sp.
 (iii) NUMBER OF SEQUENCES: 2
 (iv) CORRESPONDENCE ADDRESS:
 (A) ADDRESSEE: Smith and Jones
 (B) STREET: 123 Main Street
 (C) CITY: Smalltown
 (D) STATE: Anystate
 (E) COUNTRY: USA
 (F) ZIP: 12345
 (v) COMPUTER READABLE FORM:
 (A) MEDIUM TYPE: Diskette, 3.50 inch, 800 Kb storage
 (B) COMPUTER: Apple Macintosh
 (C) OPERATING SYSTEM: McIntosh 5.0
 (D) SOFTWARE: MacWrite
 (vi) CURRENT APPLICATION DATA:
 (A) APPLICATION NUMBER: 09/999,999
 (B) FILING DATE: 28-FEB-1989
 (C) CLASSIFICATION: 999/99
 (vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: PCT/US88/99999
 (B) FILING DATE: 01-MAR-1988
 (viii) ATTORNEY/AGENT INFORMATION:
 (A) NAME: Smith, John A.
 (B) REGISTRATION NUMBER: 00001
 (C) REFERENCE/DOCKET NUMBER: 01-0001
 (ix) TELECOMMUNICATION INFORMATION:
 (A) TELEPHONE: (909) 999-0001
 (B) TELEFAX: (909) 999-0002
 (2) INFORMATION FOR SEQ ID NO: 1:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 954 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (iii) HYPOTHETICAL: yes
 (iv) ANTI-SENSE: no
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Paramecium* sp
 (C) INDIVIDUAL/ISOLATE: XYZ2
 (G) CELL TYPE: unicellular organism
 (vii) IMMEDIATE SOURCE:
 (A) LIBRARY: genomic
 (B) CLONE: Para-XYZ2/36
 (x) PUBLICATION INFORMATION:
 (A) AUTHORS: Doe, Joan X. Doe, John Q
 (B) TITLE: Isolation and Characterization of a Gene Encoding a-Protease from *Paramecium* sp.
 (C) JOURNAL: Fictional Genes
 (D) VOLUME: 1
 (E) ISSUE: 1
 (F) PAGES: 1-20
 (G) DATE: 02-MAR-1988
 (K) RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 954

BILLING CODE 3510-16-M

ATCGGGATAG TACTGGTCAA GACCGGTGGA CACCGGTAA CCCCGGTAA GTACCGGTTA 60
TAGGCCATTT CAGGCCAAAT GTGCCCAACT ACGCCAATTG TTTTGCCAAC GGGCAACGTT 120
ACGTTCGTAC GCACGTATGT ACCTAGGTAC TTACGGACGT GACTACGGAC ACTTCGGTAC 180
GTACGTACGT TTACGTACCC ATCCCAACGT AACCACAGTG TGGTCGCAGT GTCCCAGTGT 240
ACACAGACTG CCAGACATTC TTCACAGACA CCCC ATG ACA CCA CCT GAA CGT CTC 295
Met Thr Pro Pro Glu Arg Leu
-30

TTC CTC CCA AGG GTG TGT GGC ACC ACC CTA CAC CTC CTC CTT CTG GGG 343
Phe Leu Pro Arg Val Cys Gly Thr Thr Leu His Leu Leu Leu Leu Gly
-25 -20 -15

CTG CTG CTG GTT CTG CTG CCT GGG GCC CAT GTGAGGCAGC AGGAGAATGG 393
Leu Leu Leu Val Leu Leu Pro Gly Ala His
-10 -5

GGTGGCTCAG CCAAACCTTG AGCCCTAGAG CCCCCCTCAA CTCTGTTCTC CTAG GGG 450
Gly

CTC ATG CAT CTT GCC CAC AGC AAC CTC AAA CCT GCT GCT CAC CTC ATT 498
Leu Met His Leu Ala His Ser Asn Leu Lys Pro Ala Ala His Leu Ile
1 5 10 15

GTAAACATCC ACCTGACCTC CCAGACATGT CCCCACCAGC TCTCCTCCTA CCCCTGCCTC 558

AGGAACCCAA GCATCCACCC CTCTCCCCCA ACTTCCCCCA CGCTAAAAAA AACAGAGGGA 618

GCCCACTCCT ATGCCTCCCC CTGCCATCCC CCAGGAACTC AGTTGTTTCAG TGCCCACTTC 678

TAC CCC AGC AAG CAG AAC TCA CTG CTC TGG AGA GCA AAC ACG GAC CGT 726
Tyr Pro Ser Lys Gln Asn Ser Leu Leu Trp Arg Ala Asn Thr Asp Arg
20 25 30

GCC TTC CTC CAG GAT GGT TTC TCC TTG AGC AAC AAT TCT CTC CTG GTC 774
Ala Phe Leu Gln Asp Gly Phe Ser Leu Ser Asn Asn Ser Leu Leu Val
35 40 45

TAGAAAAAAT AATTGATTTC AAGACCTTCT CCCCATTTCTG CCTCCATTCT GACCATTTC 834

GGGGTCGTCA CCACCTCTCC TTTGGCCATT CCAACAGCTC AAGTCTTCCC TGATCAAGTC 894

ACCGGAGCTT TCAAAGAAGG AATTCTAGGC ATCCCAGGGG ACCCACACCT CCCTGAACCA 954

(2) INFORMATION FOR SEQ ID NO: 2:	(C) IDENTIFICATION METHOD: similarity to other signal sequences, hydrophobic	(C) JOURNAL: Fictional Genes
(i) SEQUENCE CHARACTERISTICS:	(D) OTHER INFORMATION: expresses protease	(D) VOLUME: 1
(A) LENGTH: 82 amino acids	(x) PUBLICATION INFORMATION:	(E) ISSUE: 1
(B) TYPE: amino acid	(A) AUTHORS: Doe, Joan X. Doe, John Q	(F) PAGES: 1-20
(D) TOPOLOGY: linear	(B) TITLE: Isolation and Characterization of a Gene Encoding a Protease from <i>Paramecium</i> sp.	(G) DATE: 02-MAR-1988
(ii) MOLECULE TYPE: protein		(K) RELEVANT RESIDUES IN SEQ ID NO: 2: FROM -34 TO 48
(ix) FEATURE:		BILLING CODE 2510-10-M
(A) NAME/KEY: signal sequence		
(B) LOCATION: -34 to -1		

Here's where sequence 2 starts (after the sequence data of SEQ ID NO:1:)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Thr Pro Pro Glu Arg Leu Phe Leu Pro Arg Val Cys Gly Thr Thr
-30 -25 -20

Leu His Leu Leu Leu Gly Leu Leu Leu Val Leu Leu Pro Gly Ala
-15 -10 -5

His Gly Leu Met His Leu Ala His Ser Asn Leu Lys Pro Ala Ala His
1 5 10

Leu Ile Tyr Pro Ser Lys Gln Asn Ser Leu Leu Trp Arg Ala Asn Thr
15 20 25 30

Asp Arg Ala Phe Leu Gln Asp Gly Phe Ser Leu Ser Asn Asn Ser Leu
35 40 45

Leu Val

BILLING CODE 3510-16-C